



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 10-227-1011

TO: Phillip Gabel
Location: CM1/8B03/9E12
Art Unit: 1644
Wednesday, October 08, 2003

Case Serial Number: 09/454651

From: Edward Hart
Location: Biotech-Chem Library
CM1-6B02
Phone: 305-9203

edward.hart@uspto.gov

Search Notes

Examiner Gabel,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

STIC-Biotech/ChemLib

115367

From: STIC-ILL
S nt: Monday, October 06, 2003 6:39 AM
To: STIC-Biotech/ChemLib
Subject: FW: 09 / 454651 ifw amd

-----Original Message-----

Fr m: Gambel, Phillip
Sent: Saturday, October 04, 2003 9:43 AM
T : STIC-ILL
Subject: 09 / 454651 ifw amd

stic

please perform a sequence and a sequence interference search for

09 / 454,651 (ifw amd b7)

in PAPER

SEQ ID NO: 23

thanx

phillip gambel
art unit 1644
308-3997

1644 mailbox 9e12

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 10/9/03
Date Completed: 10/8/03
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 12
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 7, 2003, 10:45:40 ; Search time 67 Seconds

(without alignments)
510.060 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149

Sequence: 1 GLSHFCSGVHVTKEYVEA.....LRVNTFNNTTKQHFPPD 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	226	10	US-09-915-789A-21
2	1149	100.0	288	8	US-08-592-711-2
3	1149	100.0	288	9	US-09-772-102-14
4	1149	100.0	288	9	US-09-837-867A-19
5	1149	100.0	288	10	US-09-910-174A-5
6	1149	100.0	288	10	US-09-896-738-10
7	1149	100.0	288	10	US-09-915-789A-15
8	1149	100.0	288	11	US-09-962-969-19
9	1149	100.0	288	11	US-09-350-202-2
10	1149	100.0	288	12	US-10-032-214-278
11	1149	100.0	288	12	US-10-126-088-2
12	1149	100.0	288	12	US-10-041-319-7
13	1149	100.0	288	13	US-10-261-101-2
14	1149	100.0	473	10	US-09-910-059-131
15	1143	99.5	492	10	US-09-845-899A-3

16	1129	98.3	288	12	US-10-032-214-94	Sequence 94, Appl
17	1121	97.6	288	12	US-10-032-214-69	Sequence 69, Appl
18	1121	97.6	288	12	US-10-032-214-82	Sequence 82, Appl
19	1119	97.4	288	12	US-10-032-214-71	Sequence 71, Appl
20	1119	97.4	288	12	US-10-032-214-77	Sequence 77, Appl
21	1119	97.4	288	12	US-10-032-214-225	Sequence 225, Appl
22	1118	97.3	288	12	US-10-032-214-84	Sequence 84, Appl
23	1116	97.1	288	12	US-10-032-214-76	Sequence 76, Appl
24	1116	97.1	288	12	US-10-032-214-87	Sequence 86, Appl
25	1116	97.1	288	12	US-10-032-214-87	Sequence 87, Appl
26	1116	97.1	288	12	US-10-032-214-286	Sequence 286, Appl
27	1114	97.0	288	12	US-10-032-214-226	Sequence 226, Appl
28	1114	97.0	288	12	US-10-032-214-251	Sequence 251, Appl
29	1113	96.9	288	12	US-10-032-214-90	Sequence 90, Appl
30	1113	96.9	288	12	US-10-032-214-228	Sequence 228, Appl
31	1113	96.9	288	12	US-10-032-214-250	Sequence 250, Appl
32	1112	96.8	288	12	US-10-032-214-78	Sequence 78, Appl
33	1112	96.8	288	12	US-10-032-214-248	Sequence 248, Appl
34	1111	96.7	288	12	US-10-032-214-238	Sequence 238, Appl
35	1110	96.6	288	12	US-10-032-214-236	Sequence 236, Appl
36	1109	96.5	288	12	US-10-032-214-88	Sequence 88, Appl
37	1109	96.5	288	12	US-10-032-214-89	Sequence 89, Appl
38	1109	96.5	288	12	US-10-032-214-92	Sequence 92, Appl
39	1109	96.5	288	12	US-10-032-214-249	Sequence 249, Appl
40	1108	96.4	287	12	US-10-032-214-243	Sequence 243, Appl
41	1105	96.2	288	12	US-10-032-214-81	Sequence 81, Appl
42	1104	96.1	300	12	US-10-032-214-74	Sequence 74, Appl
43	1104	96.1	300	12	US-10-032-214-232	Sequence 232, Appl
44	1103	96.0	288	12	US-10-032-214-91	Sequence 91, Appl
45	1103	96.0	288	12	US-10-032-214-229	Sequence 229, Appl

ALIGNMENTS

RESULT 1
US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE OF INVENTION: MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match 100.0%; Score 1149; DB 10; Length 226;
Best Local Similarity 100.0%; Pred. No. 6.3e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GLSHFCSGVHVTKEYVEA	12	US-10-032-214-94	Sequence 94, Appl
DB	11	GLSHFCSGVHVTKEYVEA	12	US-10-032-214-82	Sequence 82, Appl
QY	61	YKNTFIDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTL	120	US-10-032-214-77	Sequence 77, Appl
DB	71	YKNTFIDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTL	130	US-10-032-214-84	Sequence 84, Appl
QY	121	ISDFEPTSNIRRIICSTSGGPPPEHLNLENGEELNAINTVSDPETEL	180	US-10-032-214-76	Sequence 76, Appl
DB	131	ISDFEPTSNIRRIICSTSGGPPPEHLNLENGEELNAINTVSDPETEL	190	US-10-032-214-87	Sequence 86, Appl
QY	181	NMTTNHSMFLIKYGLHVRVNTQNTKQHFPPD	216	US-10-032-214-87	Sequence 87, Appl

DB 191 NMTNHSFMCILKYGLRVNQTWNMTTKQHFDPD 226

|||||

US-08-592-711-2

RESULT 2

Sequence 2, Application US/08592711

Publication No. US20020113214A1

GENERAL INFORMATION:

APPLICANT: June, Carl H.

APPLICANT: Thompson, Craig B.

APPLICANT: Nabel, Gary J.

APPLICANT: Gray, Gary S.

APPLICANT: Rennert, Paul D.

TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/592,711

FILING DATE: 26-JAN-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,816

FILING DATE: 4-MAY-1995

APPLICATION NUMBER: US 08/403,253

FILING DATE: 10-MARCH-1995

APPLICATION NUMBER: US 08/253,964

FILING DATE: 3-JUNE-1994

APPLICATION NUMBER: US 08/073,223

FILING DATE: 4-JUNE-1993

APPLICATION NUMBER: US 08/200,947

FILING DATE: 23-FEB-1994

APPLICATION NUMBER: US 07/864,805

FILING DATE: 7-APR-1992

APPLICATION NUMBER: US 08/247,505

FILING DATE: 23-MAY-1994

APPLICATION NUMBER: US 07/864,866

FILING DATE: 7-APR-1992

APPLICATION NUMBER: US 08/218,155

FILING DATE: 25-MAR-1994

APPLICATION NUMBER: US 07/864,807

FILING DATE: 7-APR-1992

APPLICATION NUMBER: US 07/902,467

FILING DATE: 16-JUNE-1992

APPLICATION NUMBER: US 07/275,433

FILING DATE: 23-NOV-1988

ATTORNEY/AGENT INFORMATION:

NAME: Mandragouras, Amy E.

REGISTRATION NUMBER: 36,207

REFERENCE/DOCKET NUMBER: RPI-002CP4

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 288 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

DESCRIPTION: B cell activation antigen; natural ligand

FEATURE: for CD28 T cell surface antigen; transmembrane protein

NAME/KEY: signal sequence

LOCATION: -34 to -1

IDENTIFICATION METHOD: amino terminal sequencing of

IDENTIFICATION METHOD: soluble protein

OTHER INFORMATION: hydrophobic

FEATURE:

NAME/KEY: extracellular domain

LOCATION: 1 to 208

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: transmembrane domain

LOCATION: 209 to 235

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: intracellular domain

LOCATION: 236 to 254

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 19 to 21

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 55 to 57

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 64 to 66

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 152 to 154

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 173 to 175

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 177 to 179

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 192 to 194

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: N-linked glycosylation

LOCATION: 198 to 200

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig V-set domain

LOCATION: 1 to 104

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

FEATURE:

NAME/KEY: Ig C-set domain

LOCATION: 105 to 202

IDENTIFICATION METHOD: similarity with known

IDENTIFICATION METHOD: sequence

PUBLICATION INFORMATION:

AUTHORS: FREEMAN, GORDON J.

AUTHORS: FREEDMAN, ARNOLD S.

AUTHORS: SEGIL, JEFFREY M.

AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-08-592-711-2

Query Match 100.0%; Score 1149; DB 8; Length 288;
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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSEELAQTRIIYQKEKKMWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSQDPETELYAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSQDPETELYAVSSKLDF 206
QY 181 NMTTNHSPMCLIKYGHRLRVNQTENNNTTKQEHFPDN 216
DB 207 NMTTNHSPMCLIKYGHRLRVNQTENNNTTKQEHFPDN 242

RESULT 3
US-09-772-102-14
Sequence 14, Application US/09772102
Patent No. US20020006413A1
GENERAL INFORMATION:
APPLICANT: Sobol, Robert, E.
APPLICANT: Shawler, Daniel L.
APPLICANT: Bartholomew, Richard M.
APPLICANT: Carlo, Dennis J.
APPLICANT: Gold, Daniel P.
TITLE OF INVENTION: Genetically Engineered Tumor Cell
FILE REFERENCE: P-SO 4581
CURRENT APPLICATION NUMBER: US/09/772,102
PRIORITY FILING DATE: 2001-01-26
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/178,498
PRIOR FILING DATE: 2000-02-28
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-09-772-102-14

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Best Local Similarity 100.0%; Pred. No. 8.8e-103;
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DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSQDPETELYAVSSKLDF 206
QY 181 NMTTNHSPMCLIKYGHRLRVNQTENNNTTKQEHFPDN 216
DB 207 NMTTNHSPMCLIKYGHRLRVNQTENNNTTKQEHFPDN 242
RESULT 4
US-09-837-867A-19
Sequence 19, Application US/09837867A
Patent No. US20020098542A1
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Hortiello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. US20020098542A1el Forms of T Cell Costimulatory
FILE REFERENCE: BWI-120CPADY
CURRENT APPLICATION NUMBER: US/09/837,867A
PRIORITY FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 08/205,697
PRIOR FILING DATE: 1994-03-02
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 19
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-09-837-867A-19

Query Match 100.0%; Score 1149; DB 9; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVVLYEKDAFKREHLAEVTLVKADFTPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSQDPETELYAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINITVSQDPETELYAVSSKLDF 206
QY 181 NMTTNHSPMCLIKYGHRLRVNQTENNNTTKQEHFPDN 216
DB 207 NMTTNHSPMCLIKYGHRLRVNQTENNNTTKQEHFPDN 242

RESULT 5
US-09-910-174A-5
Sequence 5, Application US/09910174A
Patent No. US20020106730A1
GENERAL INFORMATION:
APPLICANT: Coyle, Anthony J.
APPLICANT: Fraser, Christopher C.
APPLICANT: Manning, Stephen
TITLE OF INVENTION: B7-H2 Molecules, No. US20020106730A1el Members of the B7
FILE REFERENCE: 35800/236924
CURRENT APPLICATION NUMBER: US/09/910,174A
PRIORITY FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: US 09/620,461
PRIOR FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FastSeq for Windows version 4.0
SEQ ID NO 5
LENGTH: 288

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174A-5

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Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKKWLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDITNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDLF 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 216
DB 207 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 242

RESULT 6
US-09-896-738-10
; Sequence 10, Application US/09896738
; Patent No. US2002016347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; APPLICANT: Fang, Mei
; TITLE OF INVENTION: B7-Like Molecules and Uses Thereof
; FILE REFERENCE: 00-513-A
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 10
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-738-10

Query Match      100.0%; Score 1149; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKKWLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDITNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDLF 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 216
DB 207 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 242

RESULT 7
US-09-915-789A-15
; Sequence 15, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
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; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-15

Query Match      100.0%; Score 1149; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKKWLTMMSGDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIYWQEKKKWLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNTIFDITNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDLF 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 216
DB 207 NMTNHSFMCCLKYGHRLVNOTFNNTTKQEHFPDN 242

RESULT 8
US-09-962-969-19
; Sequence 19, Application US/09962969
; Publication No. US20030045703A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; Borriello, Francescopaolo
; Freeman, Gordon
; Nadler, Lee
; TITLE OF INVENTION: No. US20030045703A1e1 Forms of T Cell Costimulatory
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS: Molecules and Uses Therefor
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,969
; FILING DATE: 24-Sep-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/702,525
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
```


NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEDMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
US-09-350-202-2

Query Match 100.0%; Score 1149; DB 11; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIIYQKEKKKWLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIIYQKEKKKWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDIINLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 67 YKNRTIFDIINLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLRVNQTFNNNTTKQEHFPDN 216
DB 207 NMTNHSFMCILIKYGLRVNQTFNNNTTKQEHFPDN 242

RESULT 10
US-10-032-214-278
Sequence 278, Application US/10032214
Publication No. US20030138881A1
GENERAL INFORMATION:
APPLICANT: FUNNEN, JUHA
APPLICANT: LAZETIC, ALEXANDRA
APPLICANT: LEONG, STEVEN R.
APPLICANT: CHANG, CHIA-CHUN
APPLICANT: APT, DORIS
APPLICANT: GUSTAFSSON, CLAES
TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
FILE REFERENCE: 02-106730US
CURRENT APPLICATION NUMBER: US/10/032.214
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 09/888,324

PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: PCT/US01/19973
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,946
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/241,245
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 320
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 278
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-214-278
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIIYQKEKKKWLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVHVTKVEKVAITLSCGHNVSVEELAQTRIIYQKEKKKWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDIINLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKNRTIFDIINLSIVILALRPSDEGTVECVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 180
DB 147 ISDFEPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTVSQDPETELYAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLRVNQTFNNNTTKQEHFPDN 216
DB 207 NMTNHSFMCILIKYGLRVNQTFNNNTTKQEHFPDN 242
RESULT 11
US-10-126-088-2
Sequence 2, Application US/10126088
Publication No. US20030170821A1
GENERAL INFORMATION:
APPLICANT: FREEDMAN, GORDON J.
NADLER, LEE M.
TITLE OF INVENTION: DNA Encoding B7, A New Member
Of The Ig Superfamily With Unique Expression On
Activated And Neoplastic B Cells.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM personal system 2; Model 30
OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/126,088
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
APPLICATION NUMBER: US 07/591,300
FILING DATE: 01-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig V-set domain

LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J., FREEDMAN, ARNOLD S., SEGIL, JEFFREY M., LEE, GRACE, WHITMAN, JAMES F., NADLER, LEE M., A New Member Of the Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUFS IN SEQ ID NO: 2: From -26 to 262
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-126-088-2
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 216; Conservative 0;
Qy 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKMKVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKMKVLTMMSGDMNIWPE 86
Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGYCVLKYKDAFKREHLAEVTLVKADFPPTS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTGYCVLKYKDAFKREHLAEVTLVKADFPPTS 146
Qy 121 ISDFEPTSNIRRICSTSGFPPEHLSWLENELNAINTTVSQDPETELVAVSSKIDF 180
Db 147 ISDFEPTSNIRRICSTSGFPPEHLSWLENELNAINTTVSQDPETELVAVSSKIDF 206
Qy 181 NMTNHSFMCLIKYGHRLVRVNTFNWNTTKQHFDPN 216
Db 207 NMTNHSFMCLIKYGHRLVRVNTFNWNTTKQHFDPN 242
RESULT 12
US-10-041-319-7
; Sequence 7, Application US/10041319
; Publication No. US20030180309A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Baum, Peter R.
; APPLICANT: DuBose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HUMAN B7 POLYPEPTIDES
; FILE REFERENCE: 3176-A
; CURRENT APPLICATION NUMBER: US/10/041,319
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-041-319-7
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 216; Conservative 0;
Qy 1 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKMKVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIVWQEKKMKVLTMMSGDMNIWPE 86

QY 61 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLVSLWENGEELNAINTVSQDPETELVAVSSKLD 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLVSLWENGEELNAINTVSQDPETELVAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHVRVNOTFNWNTTKEHFPDN 216
DB 207 NMTNHSFMCILIKYGLHVRVNOTFNWNTTKEHFPDN 242

RESULT 13

US-10-261-101-2
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
Baskar, Sivasubramanian
Glimcher, Laurie H.
Freeman, Gordon J.
Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/261.101
FILING DATE: 30-Sep-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/966.148
FILING DATE: 27-Sep-2000
APPLICATION NUMBER: 08/147.772
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 1149; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 8.8e-103;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVBELAQRIYQKKEKVVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVBELAQRIYQKKEKVVLTMMSGDMNIWPE 86
QY 61 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLVSLWENGEELNAINTVSQDPETELVAVSSKLD 180

DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLVSLWENGEELNAINTVSQDPETELVAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHVRVNOTFNWNTTKEHFPDN 216
DB 207 NMTNHSFMCILIKYGLHVRVNOTFNWNTTKEHFPDN 242
RESULT 14
US-09-910-059-131
Sequence 131, Application US/09910059
Patent No. US20020142359A1
GENERAL INFORMATION:
APPLICANT: Copley, Clive G
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibod
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910.059
CURRENT FILING DATE: 2001-07-23
PRIOR FILING DATE: 09/171.945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 131
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

Query Match 100.0%; Score 1149; DB 10; Length 473;
Best Local Similarity 100.0%; Pred. No. 1.7e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVATLSCGHNVSVBELAQRIYQKKEKVVLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVATLSCGHNVSVBELAQRIYQKKEKVVLTMMSGDMNIWPE 86
QY 61 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKRTIFDITNNLSIVILALRPSDEGTGECVVLKYKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLVSLWENGEELNAINTVSQDPETELVAVSSKLD 180
DB 147 ISDFEIPTSNIRRIICSTSGGFPPEHLVSLWENGEELNAINTVSQDPETELVAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLHVRVNOTFNWNTTKEHFPDN 216
DB 207 NMTNHSFMCILIKYGLHVRVNOTFNWNTTKEHFPDN 242

RESULT 15

US-09-845-899A-3
Sequence 3, Application US/09845899A
Patent No. US20020147326A1
GENERAL INFORMATION:
APPLICANT: CHAIKIN, MARGERY ANN
APPLICANT: LYN, SALLY DOREEN PATRICIA
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TRUNEH, ALEMEGER
TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P50496
CURRENT APPLICATION NUMBER: US/09/845.899A

; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/202,346
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/043,948
; PRIOR FILING DATE: 1997-02-19
; PRIOR APPLICATION NUMBER: US 60/038,915
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 492
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-845-899A-3

Query Match 99.5%; Score 1143; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 6.9e-102;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVDELAQTRIYWQEKKKVLTMMSCDMNIWPE 60
DB 27 GLSHFCGVIHVTKEVATLSCGHNVSVDELAQTRIYWQEKKKVLTMMSCDMNIWPE 80
QY 61 YKRTIFDITNNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 120
DB 87 YKRTIFDITNNLSIVILALRPSDEGTYECVYLKYEKDAFKREHLAEVTLVKADFPPTS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGELNAINTVSQDPETELYAVSSKLDF 180
DB 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGELNAINTVSQDPETELYAVSSKLDF 206
QY 181 NMTNHSEFMCLIKYGHILRVNOTFNWNTTKOEHPD 215
DB 207 NMTNHSEFMCLIKYGHILRVNOTFNWNTTKOEHPD 241

Search completed: October 7, 2003, 10:55:28
Job time : 68 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: October 7, 2003, 10:33:15 ; Search time 23 seconds

(without alignments)
441.642 Million cell updates/sec

Title: US-09-454-651b-23

Perfect score: 1149

Sequence: 1 GLSHFCGVIHVTKEYEVA.....LRVNOTFNWNTTQEHFDPN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	100.0	288	1	CD80_HUMAN
2	738	64.2	299	1	CD80_RABIT
3	561	48.8	306	1	CD80_MOUSE
4	182	15.8	329	1	CD86_HUMAN
5	161	14.0	302	1	ICOL_HUMAN
6	152	13.2	309	1	CD86_MOUSE
7	150.5	13.1	322	1	ICOL_MOUSE
8	140.5	12.2	330	1	CD86_RABIT
9	138	12.0	509	1	SHS1_RAT
10	134.5	11.7	583	1	CL166_MOUSE
11	133.5	11.6	583	1	CL166_HUMAN
12	129	11.2	221	1	BRF1_EBV
13	127	11.1	526	1	BUTY_HUMAN
14	122.5	10.7	588	1	CL166_CHICK
15	120.5	10.5	513	1	SHS1_MOUSE
16	120	10.4	506	1	SHS1_BOVIN
17	119	10.4	524	1	BUTY_MOUSE
18	116.5	10.1	1088	1	NCA1_XENLA
19	115	10.0	761	1	NCA2_HUMAN
20	115	10.0	848	1	NCA1_HUMAN
21	110.5	9.6	321	1	TCR_EBV
22	110	9.6	398	1	SRB1_HUMAN
23	109.5	9.5	646	1	MU18_HUMAN
24	109.5	9.5	853	1	NCA1_BOVIN
25	109	9.5	387	1	SRB2_MOUSE
26	109	9.5	526	1	BUTY_BOVIN
27	109	9.5	2029	1	LAR_DROME
28	108.5	9.4	365	1	CD80_MOUSE
29	107.5	9.4	333	1	AMAL_DROME
30	106.5	9.3	858	1	NCA1_RAT
31	105	9.1	319	1	A33_HUMAN
32	105	9.1	1091	1	NCA1_CHICK
33	104	9.1	1092	1	NCA2_XENLA

34	103.5	9.0	725	1	NCA2_MOUSE	P13594 mus musculus
35	103.5	9.0	1115	1	NCA1_MOUSE	P13595 mus musculus
36	103	8.9	298	1	JAM2_HUMAN	P57087 homo sapien
37	102.5	8.9	503	1	SHS1_HUMAN	P78324 h proteint
38	102	8.9	1443	1	NEOL_CHICK	Q90610 gallus gall
39	101.5	8.8	403	1	RAGE_MOUSE	Q62151 mus musculus
40	100	8.7	413	1	HEMO_MANSE	P31398 manduca soc
41	99.5	8.7	1338	1	VGRI_HUMAN	P17948 h vascular
42	98.5	8.6	365	1	CXAR_HUMAN	P78310 homo sapien
43	98.5	8.6	1242	1	NPHN_MOUSE	Q9qz57 mus musculus
44	98	8.5	278	1	OX2G_RAT	P04218 rattus norv
45	98	8.5	298	1	JAM1_BOVIN	Q9xt56 bos taurus

ALIGNMENTS

CD80_HUMAN						
1D	CD80_HUMAN	STANDARD:	PRT;	288	AA.	
AC	P33681:					
DT	01-FEB-1994 (Rel. 28, Created)					
DT	01-FEB-1994 (Rel. 28, Last sequence update)					
DT	15-SEP-2003 (Rel. 42, Last annotation update)					
DE	T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BBI).					
GN	CD80 OR CD28LG1 OR CD28LG OR LAB7.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	TISSUE=Lymphoid;					
RX	MEDLINE=90010147; PubMed=2794510;					
RA	Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F.,					
RA	Nadler L.M.;					
RT	"B7, a new member of the Ig superfamily with unique expression on					
RT	activated and neoplastic B cells.";					
RL	J. Immunol. 143:2714-2722(1989).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=92307753; PubMed=1377173;					
RA	Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C.,					
RA	Dupont B.;					
RT	"Genomic organization and chromosomal location of the human gene					
RT	encoding the B-lymphocyte activation antigen B7.";					
RL	Immunogenetics 36:175-181(1992).					
RN	[3]					
RP	SEQUENCE OF 35-38.					
RX	MEDLINE=91341422; PubMed=1714935;					
RA	Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J.,					
RA	White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;					
RT	"Structure, expression, and T cell costimulatory activity of the					
RT	murine homologue of the human B lymphocyte activation antigen B7.";					
RL	J. Exp. Med. 174:625-631(1991).					
RN	[4]					
RP	CHARACTERIZATION.					
RX	MEDLINE=95088403; PubMed=7527824;					
RA	Larier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,					
RA	Okumura K., Ito D., Azuma M.;					
RT	"CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T					
RT	cell proliferation, cytokine production, and generation of CTL.";					
RL	J. Immunol. 154:97-105(1995).					
RN	[5]					
RP	X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.					
RX	MEDLINE=20125021; PubMed=10661405;					
RA	Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K.,					
RA	Jones E.Y., Stuart D.I., Davis S.J.;					
RT	"Structure and dimerization of a soluble form of B7-1.";					
RL	Immunology 12:51-60(2000).					
CC	!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T					
CC	LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE					

CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, MACROPHAGES
 CC AND DENDRITIC CELLS.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- DATABASE: NAME=PROM; NOTE=CD guide CD80 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd80.htm".
 CC -----
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 CC -----
 CC EMBL; M27533; AAA36045.1; -.
 CC EMBL; M83077; AAA58390.1; -.
 CC EMBL; M83072; AAA58390.1; JOINED.
 CC EMBL; M83073; AAA58390.1; JOINED.
 CC EMBL; M83074; AAA58390.1; JOINED.
 CC PIR; I54495; A45803.
 CC PDB; 1DR9; 10-JAN-01.
 CC PDB; 118L; 04-APR-01.
 CC Genew; HGNC:1700; CD80.
 CC MIM; 112203; -.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003599; Ig.
 CC InterPro; IPR003006; Ig_MHC.
 CC Pfam; PF00047; Ig; 1.
 CC SMART; SM00409; Ig; 1.
 CC PROSITE; PS00835; IG-LIKE; 2.
 CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor; 3D-structure.
 FT SIGNAL 1 34
 FT CHAIN 35 288
 FT DOMAIN 35 242 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
 FT TRANSMEM 243 263 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 264 288 POTENTIAL.
 FT DOMAIN 35 135 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 145 230 IG-LIKE V-TYPE.
 FT DISULFID 50 116 IG-LIKE C2-TYPE.
 FT DISULFID 162 216
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 89 89 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 207 207 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 226 226 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 232 232 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT STRAND 37 41
 FT TURN 42 43
 FT STRAND 46 48
 FT TURN 56 57
 FT TURN 58 61
 FT HELIX 61 68
 FT STRAND 63 68
 FT TURN 69 70
 FT STRAND 71 77
 FT TURN 77 79
 FT STRAND 80 83
 FT STRAND 85 88
 FT HELIX 88 90
 FT TURN 89 90
 FT STRAND 91 94
 FT TURN 96 99
 FT STRAND 100 103
 FT TURN 108 110
 FT HELIX 110 120
 FT STRAND 112 120
 FT TURN 123 124
 FT STRAND 127 139
 FT STRAND 146 151

FT TURN 155 156
 FT STRAND 157 167
 FT STRAND 171 177
 FT STRAND 181 182
 FT STRAND 186 191
 FT TURN 193 195
 FT STRAND 198 207
 FT TURN 208 209
 FT STRAND 212 220
 FT TURN 221 222
 FT STRAND 225 231
 FT STRAND 288 AA; 33048 MW; BA453EE34528B1F4 CRC64;
 SQ SEQUENCE 288 AA; 33048 MW; BA453EE34528B1F4 CRC64;
 Query Match 100.0%; Score 1149; DB 1; Length 288;
 Best Local Similarity 100.0%; Pred. No. 1.7e-88;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 1 GLSHPCSVIHVTKEVKEVATLSGCHNVSVLELAQTRIIYQKKEKMYLTMMSCDMNIWPE 60
 DB 27 GLSHFCSGVHVTKVKEVATLSGCHNVSVLELAQTRIIYQKKEKMYLTMMSCDMNIWPE 86
 QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLYKYEKDAFKREHLAEVTLISVKADFPPTS 120
 DB 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLYKYEKDAFKREHLAEVTLISVKADFPPTS 146
 QY 121 ISDFEIPTSNIRRIICSTISGGFPEPHLSWLENGELNAINITVSDPETELIYAVSSKLD 180
 DB 147 ISDFEIPTSNIRRIICSTISGGFPEPHLSWLENGELNAINITVSDPETELIYAVSSKLD 206
 QY 181 NMTNHSFMCILIKYGHRLVNOTFNNTTKQHFHFDN 216
 DB 207 NMTNHSFMCILIKYGHRLVNOTFNNTTKQHFHFDN 242

 RESULT 2
 CD80_RABIT STANDARD; PRT; 299 AA.
 ID CD80_RABIT
 AC P42070;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
 DE antigen).
 DE CD80.
 GN CD80.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID:9986;
 RN 111
 RP SEQUENCE FROM N.A.
 RC STRAIN-B/J X CHBB:HM;
 RX MEDLINE:95369849; PubMed-7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules.";
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
 CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
 CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
 CC RECEPTOR.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -----
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 CC EMBL; D49843; BAA08643.1; -.

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OM protein - protein search, using sw model

Run on: October 7, 2003, 10:40:10 ; Search time 96 Seconds

(without alignments)
580.618 Million cell updates/sec

Title: US-09-454-651B-23

Perfect score: 1149

Sequence: 1 GLSHFGSGVHVTKEVKEVA.....LRVNTQFNNTTKQEHFQDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phase:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-rviro:*
- 16: sp-bacteriap:*
- 17: sp-archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1118	97.3	288	6	077684
2	1100	95.7	288	6	Q28499
3	1085	94.4	288	6	Q9BDN6
4	1085	94.4	289	6	Q28347
5	772	67.2	296	6	Q8WMZ2
6	764	66.5	230	6	Q9N213
7	762.5	66.4	288	6	Q9TT70
8	762.5	66.4	297	6	Q9BE99
9	761	66.2	229	6	Q9TT71
10	743	64.7	292	6	Q9GM28
11	743	64.7	292	6	Q02758
12	719	62.6	304	6	Q9TQX1
13	717.5	62.4	296	6	Q46405
14	705	61.4	235	6	Q9N070
15	705	61.4	235	6	Q9TQ58
16	659	57.4	294	11	Q8BH36

17	603.5	52.5	321	11	035187
18	602	52.4	290	11	Q62680
19	601.5	52.3	321	11	Q62624
20	596	51.9	321	11	055202
21	560	48.7	306	11	Q9R129
22	350	30.5	174	6	Q9GM29
23	349.5	30.4	173	6	Q95L17
24	255.5	22.2	212	11	061332
25	200.5	17.4	329	6	Q9XSX6
26	200.5	17.4	332	6	Q9GM27
27	200.5	17.4	332	6	Q95L16
28	188.5	16.4	280	6	Q9TTH1
29	188.5	16.4	296	13	Q42404
30	182	15.8	329	6	Q9TTF2
31	178	15.5	323	6	Q9BDN2
32	177	15.4	323	6	Q9BDN9
33	177	15.4	323	6	Q9BDM4
34	176	15.3	275	6	Q9BDN9
35	176	15.3	323	6	Q9BDN8
36	171	14.9	284	6	Q9GL33
37	166.5	14.5	289	11	08K3J3
38	165	14.4	281	11	Q8CJ28
39	162	14.1	313	11	035531
40	161.5	14.1	325	6	Q02838
41	159	13.8	316	11	Q8V598
42	156.5	13.6	290	4	Q9NZ37
43	153	13.3	290	11	Q9EP73
44	153	13.3	356	11	Q64381
45	152	13.2	314	11	061238

ALIGNMENTS

RESULT 1

077684 PRELIMINARY; PRT; 288 AA.
 AC 077684;
 DT 01-NOV-1998 (TRENBLrel. 08, Created)
 DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
 DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
 DE B7 protein.
 GN B7.
 OS Macaca nemestrina (Pig-tailed macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
 OC Cercopitheciinae; Macaca.
 OX NCBI_TaxID=9545;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kraus G., Hnatyszyn J.H.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF079519; AAC31555.1;
 DR HSSP; P33681; 1DR9.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_1.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG-LIKE; 2.
 SQ SEQUENCE 288 AA; 33131 MW; 76BRC42839F9AR79 CRC64;

Query Match 97.3%; Score 1118; DB 6; Length 288;

Best Local Similarity 97.7%; Pred. No. 1e-92;

Matches 210; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 LSHFGSGVHVTKEVKEVATLSCGHNVSVLELAOTRIYWKQKKWLTMMSCDMNIWPEY 61

.Db 28 LSHFGSGVHVTKEVKEVATLSCGHNVSVLELAOTRIYWKQKKWLTMMSCDMNIWPEY 87

QY 62 NRTTFDITNLISVILALRPSDEGIVKVEKDAFKREHLAEVTLVSKADFPPTSI 121

.Db 88 NRTTFDITNLISVILALRPSDEGIVKVEKDAFKREHLAEVTLVSKADFPPTSI 147

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QY 122 SDPEIPTSNIIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDFEIPSPNIIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCILIKYGHRLVRNQTNNWNTTKQEHFPDN 216
DB 208 MTNHSFMCILIKYGHRLVRNQTNNWNTPKQEHFPDN 242

RESULT 2
Q28499 ID Q28499 PRELIMINARY; PRT: 288 AA.
AC Q28499;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE B7 protein (CD80 protein precursor).
GN B7 OR N939.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates.";
RL J. Immunol. 155:3946-3954(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 0:0-0(2001).
DR EMBL; U19840; AAK86706.1;
DR EMBL; AF344849; AAK37609.1;
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Signal.
FT SIGNAL 1 26 POTENTIAL.
SQ SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.7%; Score 1100; DB 6; Length 288;
Best Local Similarity 96.3%; Pred. No. 4.2e-91;
Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMMSGDMNIWPEY 61
DB 28 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMMSGDMNIWPEY 87

QY 62 KNRTIFDTNNLSIVILALRPSDEGYECVLYKYEKDAFKREHLAEVTLISKADPTPSI 121
DB 88 KNRTIFDTNNLSIVILALRPSDEGYECVLYKYEKDAFKREHLAEVTLISKADPTPSI 147

QY 122 SDPEIPTSNIIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDFEIPSPNIIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCILIKYGHRLVRNQTNNWNTTKQEHFPDN 216
DB 208 MTNHSFMCILIKYGHRLVRNQTNNWNTPKQEHFPDN 242

RESULT 3
Q9BDN6 ID Q9BDN6 PRELIMINARY; PRT: 288 AA.
AC Q9BDN6;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CD80 protein.
GN MNB71.
OS Cercocebus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercocebus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate
RT Fas/Fas-ligand and co-stimulatory molecules.";
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344839; AAK37535.1;
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG-LIKE; 1.
SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;
Best Local Similarity 95.3%; Pred. No. 9.4e-90;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMMSGDMNIWPEY 61
DB 28 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKEKKVLTMMSGDMNIWPEY 87

QY 62 KNRTIFDTNNLSIVILALRPSDEGYECVLYKYEKDAFKREHLAEVTLISKADPTPSI 121
DB 88 KNRTIFDTNNLSIVILALRPSDEGYECVLYKYEKDAFKREHLAEVTLISKADPTPSI 147

QY 122 SDPEIPTSNIIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDFEIPSPNIIRIICSTSGGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCILIKYGHRLVRNQTNNWNTTKQEHFPDN 216
DB 208 MTNHSFMCILIKYGHRLVRNQTNNWNTPKQEHFPDN 242

RESULT 4
Q28347 ID Q28347 PRELIMINARY; PRT: 289 AA.
AC Q28347;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE B7 protein (Fragment).
GN B7.
OS Cercocebus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercocebus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and

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